

	- 1				
	13		-	50 1	<del>-</del> 60
1093 422 422 507 432 207 150 2588	GGGGAAACCC GGGGAAACCC GGGGAAACCC GGGGAAACCC	AGCACGAGTG AGCACGAGTG AGCACGAGTG AGCACGAGTA AGCACGAGTA	ATGTCGTGT ATGTCGTGT ATGTCGTGT AGGTCGTGT ATGTCGTGT	TACCCGNATC TACCCGNATC GACCCAACGC TACCCGNATC TACCCGNATC	T M.paratuberc. T M.phlei
	210	22			
501 586 511 286 229	CATCTCAGTAC CATCTCAGTAC CATCTCAGTAC CATCTCAGTAC	CCGTAGGAGI CCGTAGAAGI CCGTAGGAGI CCGTAGGAGI CCGTAGGAGI	AGAAAACAA AGAAAACAA AGAAAACAA AGAAAACAA	ATTGTGATTCC ATTGTGATTCC ATTGTGATTCC ATGTGATTCC	M.paratuberc. M.phlei
	330	340	35	0 36	- 0
617 703 629 404 347	TGTGGGATTGA TGTGGGGCCTG TGTGGGATTGG TGTGGGATCGA TGTGGGATCGA	TATGTCTCAG PATGTCTCAG PATGTCTCAA PAGGTCTCAG PAGGTCTCAG	CTCTACCTG CTCTACCTG CGTCCGCCG CTCTACCTGG CTCTACCCGG CTCTACCCGG	GCTGAGG-GG GCTGAGG-GG GCGATGGCAG GITGAGG-GG GCTGAGG-GG	M.paratuberc. M.phlei M.leprae

Figure 1A





	450	460	470	480	)
1406	CGGCACCTGCCT	AGTATCAATTCCC	GAGTAGCAG	CGGGCC	M.tuberculosis
735	CGGCACCTGCCT				
	CGGCACCTGCCT	TATATCAACACCC	CGAGTAGCAG	CGGGCC	M.paratuberc.
820	TGCTGCCFGCTG	TCACAGGTCCC	CGAGTAGCAG	CGGGCC	M.phlei
747		TGTATCAATTCCC			
522	CGGCACCTGCCT				
465	CGGCACCTGCCT	TGTATCAATTCCC	CGAGTAGCAG	CGGGCC	M.kansasii
2902	CGACGTCTGTCT	TGATGGTGTTCCC	CGAGTAGCAG	CGGGCC	M.smegmatis

				<del></del>		
		490	ter Prope	500	510	520
L446	CGTGGAA	TCCCC	TGT	AATCOGO	CCGGGACCACCCG	GTAAG I
75	CGTGGAA	TCTGC	TGT	FAATCTGO	CCGGGACCACCCG	GTAAG 1
775					CCGGGACCACCCG	
857					CCGGGACCACCCG	
787					CCGGGACCACCCG	
562					CCGGGACCACCCG	
505					CGGGACCACCCG	
2942	CGTGGAA	TCTGC	TGTO	SAATCHGO	CGGGACCACCCG	GTAAG

Figure 1B



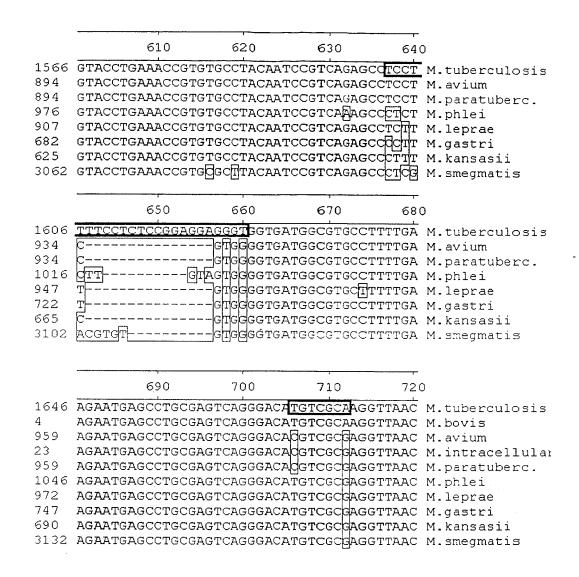


Figure 1C

A.C. FIG.

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			<del></del>			
		770	780	790	80	0
1726	CGACCCA	CACGCGCAT	ACCCCCCTCT	GAAFAGTGGC	GTGT	M.tuberculosis
84	CGACCCA	CACGCGCAT	ACGCGCGTGT	GAATAGTGGC	GTGT	M.bovis
1039	CG	CATCCCCTT	TGGGGTGT	AGTGGC		M.avium
103	CG	CATCCCTT	regerer	AGTGGC		M.intracellular
1039		CATCCTTT		AGTGGC		M.paratuberc.
1126	CGTATC	AACCTGTTG	GGGTTGGTGT	agtggfi		M.phlei
1052	CGTAT	CACGIGIGA		AGTGGC		M.leprae
827	CGTAT	CACGCGTAA	GCGHGHGT	AGTGGC		M.gastri
770	CGTAT	CGCGCGGA	GCGHGHGT	AGTGGC		M.kansasii
3212	CGTAT	CCACACAAG	AGTGTGTGGT	Gragtggf		M.smegmatis
					•	y <b>y</b>
						• • • • •
	•		1	- г		
		970	980	990	100	0
1926	ATTTAGG	TGCAGCGTT	GCGTGGTTCAG	cocceseer	DGDG	M.tuberculosis
1228	ATTTAGG	TGCAGCGTT	GCGTGGTTCAG	CCACGGAGGT	AGAG	M.avium
1228	ATTTAGG	TGCAGCGTT	GCGTGGTTCAG	CCACGGAGGT	AGAG	M.paratuberc.
1322	ATTTAGG	TGCAGCGT	GCATGNTTCT:	PATCGGAGGT	AGAG	M.phlei
1244	ATTTAGG	TGCAGCGTT	GCGTGGTTCAC	CCACGGAGGT	AGAG	M.leprae
1019	ATTTAGG	TGCAGCGTT	3CGTGNTTCAC	CCACGGAGGT	AGAG	M.gastri
962	ATTTAGG	TGCAGCGTT	GCGTGTTTCAC	CCACGGAGGT	AGAG	M.kansasii
3408	ATTTAGG	TGCAGCGTR	GCATGITTCF:	rgccggaggt:	AGAG	M.smegmatis
						···· Sincymac 15
				_		
		1050	1060	1070	108	0
2005	CAGCCAA	ACTCCGAATC	GCCG-TGGTG-	ma aabaam	2007	** ****
1307	CAGCCAA	ACTCCGAAT ACTCCGAAT	3CCG-TGGTG- 3CCG-TGGTG-	-mambaaccer	JGCA JCCA	M.tuberculosis
1307	CAGCCAA	ACTCCGAAT( ACTCCGAAT(		- IAIAAGCGI	AUDE	M.paratuberc.
	CAGCCAA	₽Ċ#ĊĊĠ₩₩Ŧſ	sccg-tggtg- sccgAtaag-	-TAMAAGCGT -TGAAAGTGT	AJUE	M.paratuberc.
1323	CAGCCAA	△○▼○○GHAT( □□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□	SCCGATIAAG SCCG-TGGTII-	- TENAMONG.	JGCA ZCC3	M.lonnes
1098	CAGCCAA	ヘ◡エ◡◡◷◬◬™ »ํᲚᲚᲚᲚᲚ™™	3CCG-4CC44		CCCA	M. reprae
1041	CAGCCAA	ACTCCCAAM ACTCCCAAM	SCCG-TGGTG-		3GCA	M.gastri M.kansasii
	CAGCCAA	ṇ◯↓◯◯GAAT( ằ◯™୯୯୯୯୭୭Ლ	-01.691.6-4		aGCA aola	M.kansasii
2400	CAGCCAA	ACICCGAAT	-CODITHAGG	~ CHARAMOTT GO	3 GMA	M.smegmatis

#### Figure 1D



		1120	1110	1150		
		1130	1140	1150	116	· ·
2082	ACAGCCC	CAGATCGC	CGGCTAAGG	CCCCC AAGCGT	GTGCTA	M.tuberculosis
1385	ACAGCCC	CAGATCGC	CGGCTAAGG	CCCCMAAGCGT	GTGCTA	M avium
1385	ACAGCCC	CAGATCGC	CGGCTAAGG	CCCCHAAGCGT	GTGCTA	M. paratubero
14/9	ACAGCCC	CAGATCGC	CGGCTAAGG	CCCCMAAGCGT	GTGCTA	Mohlei
1401	ACAGCCC	CAGATCGC	CGGCTAAGG	CCCCHAAGCGT	GTGCTA	M.lenrae
1175	ACAGCCC	CAGATCGC	CGGCTAAGG	CCCCALAAGCGT	GTGCTA	M.gastri
1118	ACAGCCC	CAGATCGC	CGGCTAAGG	CCCCAAAGCGT	GTGCTA	M.kansasii
3566	ACAGCCC	CAGATCGC	CGGNTAAGG	CCCCHAAGCGT	TTGTTA	M.smegmatis
			<del></del>	_		J
			_			
				· · · · · · · · · · · · · · · · · · ·		
		1290	1300	1310	132	0
2241	CTCAAGC	CACACCGC	CGAAGCCGC	GGCACATCCAC	СТТСТ-	M.tuberculosis
1544	CTCAAGC	CACACCGC	CGAAGCCGC	GGCACATTCAT	CTT-TA	M. avium
1544	CTCAAGC	CACACCGC	CGAAGCCGC	GGCACATTCAT		M.paratuberc.
1638	CTCAAGC	CACACCGC	CGAAGCCGC	GGCAF-ATCAG	COTHTG	M nhlei
1560	CTCAAGC	ACACCGC	CGAAGCCGC	GGCACATICAC		M.leprae
1334	CTCAAGC	ACACCGC	CGAAGCCGC	GACAFAC		M.gastri
1277	CTCAAGC	ACACCGC	CGAAGCCGC	GACAAC	1 1	M.kansasii
3726	TTCAAGO	ACACCGC	CGAAGCCGC	GGAAGCCAA		M.smegmatis
	_				-G-E-S	··· smegmacis
		1222			<del></del>	
		1330	1340	1350	136	•
2280	-GGTGGG	TGreeri	AGGGGAGCG'	TCCCTCATTCA	GCGAAG	M.tuberculosis
1583	PEGTEGA	TGTGGGT	\GGGGAGCG'	TCCCCCATTCA	GCGAAG	M.avium
1583		TGTGGGT	AGGGGAGCG'	TCCCCCATTCA	GCGAAG	M.paratuberc.
1676	TEGETEG	TGTGGGT	GGGGAGCG'	TCCFGCATCCG	STIGAAG	M.phlei
1600	GGGTGGA	TGTGGGTA	AGGGGAGCG'	TECTCATTCA	GCGAAG	M.leprae
1367	AGGTF	TGGGT	AGGGGAGCG'	TCCCTCATTCA	GCGAAG	M.gastri
1310	AGGT	TGGGTA	AGGGGAGCG'	TCCCTCATTCA	GCGAAG	M.kansasii
3764	TT	TGGGT	AGGGGAGCG'	TCCTG-ATCCG	FIGAAG	M.smegmatis
				- C		

Figure 1E



```
1370
                     1380
                              1390
                                        1400
2319 CCAC CGGGTGACCGGTGGTGGAGGGTGGGGGGGGGGGAGTGAGAAT M.tuberculosis
1640 CCTCCGGGTAACCGGTGGTGGAGGGTGGGGAAGTGAGAAT M.leprae
1402 CCGCCGGGTGACCGGTGGTGGAGGGTGAGGAGTGAGAAT M.gastri
1345 CTGCCGGGTGACCGGTGGTGGAGGGTGGGGGGGGGGGGAGTGAGAAT M.kansasii
3796 CCGCCGAGTATCGAGTGGTGGAGGGTGTGGGGAGTGAGAAT M.smegmatis
           1410
                     1420
                              1430
                                        1440
2359 GCAGGCATGAGTAGCGACAAGGCAAGTGAGAACCTTGCCC M.tuberculosis
1662 GCAGGCATGAGTAGCGAMAAGGCAAGTGAGAACCTTGCCC M.avium
1662 GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTGCCC M.paratuberc.
1756 GCAGGCATGAGTAGCGAMAAGGCAAGTGAGAACCTTMCCC M.phlei
1680 GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTGCCC M.leprae
1442 GCAGGCATGAGTAGCGAMAGGCAAGTGAGAACCTTGCCC M.gastri
1385 GCAGGCATGAGTAGCGAMAAGGCAAGTGAGAACCTTGCCC M.kansasii
3836 GCAGGCATGAGTAGCGATTAGGCAAGTGAGAACCTTOCCC M.smegmatis
           1570
                     1580
                              1590
                                        1600
2519 CGCCGTGACGAATCA-GCGGTACTAACCACCCAAAACCG M.tuberculosis
1821 СБПСССТВАПGAATCA-GCGGTACTAACCACCCAAAACCG M.avium
1821 CGTCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG M.paratuberc.
1915 CGICCOTGANGAATCICATTOTGCTAACCACCCAAAACCN M.phlei
1840 CGCCCGTGATGAATCA-GCGGTACTGACCACCCAAAACCG M.leprae
1602 CGCCCGTGATGAATCA-GCGGTACTAACCACCCAAAACCG M.gastri
1545 CGCCCGTGATGAATCA-GCGGTACTAACCACCCAAAACCG M.kansasii
3996 CGTCCATGATGAATCA-GCGGTACTAACCATCCAAAACCA M.smegmatis
```

Figure 1F



	<del></del>			
	1610	1620	1630	1640
2558	GAT-CGATCAC-TO	CCCTTCGGGG	TGTGGAGT	TTC-TGG M.tuberculosis
1860	GAT-CGACCATI-TO	CCCTTCGGGG	C-GTGGGG	TI-QGG M.avium
1860	GAT-CGACCAT-TO	CCCTTCGGGG	C-GTGGGG	TI-CGG M.paratuberc.
1955	GGG-CGATCF-ATO	CCF-TTCGGGGF	FLGTGEGG	TTG-GG M.phlei
1879	GAT-CGACCATATO	CCCTTCGGGG	OTATEGAGE	TU-CGG M.leprae
1641	GAT-CGATCAC-TO	CCCTTCGGGGG	A-GTGGAGG	TC-TGG M.gastri
1584	GAT-CGATCAC-TO	CCCTTCGGGGG	C-GTGGAGG	TC-TGG M.kansasii
4035	ACCGTGADCGCAC	TTTCGGGG	- Terree	TGGTGG M.smegmatis
			10100901	199166 Mishledmatts
	1.550			
	1650	1660	1670	1680
2594	GGCTGCGTGGGAAC	CTTCGCTGGTAG	TAGTCAAGC	GAAGGG M.tuberculosis
1896	GGCTGCGTGGGAIC	CTTCGCTGGTAG	TAGTCAAGC	AANGGG M.avium
1896	GGCTGCGTGGGA	CTTCGCTGGTAG	TAGTCAAGC	HANGGG M. paratuberc
1986	GGCTGCGTGGGA	CG-GTGGGTAG	TAGTCAAGC	GANGGG M.phlei
1917	GGCTGCGTGGGAAC	TTCGTTGGTAG	TAGTCAAGC	GANGGG M.leprae
1677	GGCTGCGTGGAGC	CTTCGCTGGTAG	TAGTCAAGC	GANGGG M.gastri
1620	GGCTGCGTGGAGC	TTCGCTGGTAG	TAGTCAAGC	GATGGG M.kansasii
4071	GGCTGCATGGGAC	CTTCGTTGGTAG	TAGTCAAGC	GATGGG M.smegmatis
		_		
	1690	1700	1710	1700
		2.00		1720
2634	-GTGACGCAGGAAG	GTAGCCGTACC	AGTCAGTGG	TAACA- M.tuberculosis
1936	-GTGACGCAGGAAG	gpagccgtacc:	AGTCAGTGG	TAATA- M.avium
1936	-GTGACGCAGGAAG	GEAGCCGTACC:	AGTCAGTGG	TAATA- M.paratuberc.
2025	-GTGACGCAGGAAG	GTAGCCGTACC:	AGTCAGTGG	TAANA- M.phlei
1957	-GTGACGCAGGAAG	GTAGCCGTACC:	AGTCAGTGG	TAATA- M.leprae
1717	-GTGACGCAGGAAG	gpagccgtacc:	AGTCAGTGG	TAANA- M.gastri
1660	-GTGACGCAGGAAG	G dagccgtacc:	AGTCAGTGG	TAATA- M.kansasii
4111	-GTGACGCAGGAAG	GTAGCCGTACC	GGTCAGTGG	TAAMA- M.smegmatis

# Figure 1G

G.

#### 8/31

		1730	1740	1750	176	0
2672	-CTGGG	GCAAGCCGC	TAGGGAGAG	CGATAGGCAA	ATCCGT	M tuberqulogia
1974 1974	t -CTGGG	GCAAGCCDC	STAGH-IAGAG(	CGATAGGCAA	ATCCGT	M attium
2063		GHAABCCHO	FTAGE HAGAGO	CGATAGGCAA HCDUDGCCDD	ATCCGT	M. paratuberc.
1995	-cTGGA	GCAAGCCC	TAGGGGAGE TAGGGAGAG	GATAGGCAA CGATAGGCAA	ATCCGT	M.leprae
1755	-Creece	GCAAGCCAC	TAGGGAGAG	CGATAGGCAA	ATCCGT	M dastri
1698 4149	CTGGG	GCAAGCCAG	TAGGGAGAG	CGATAGGCAA	ATCCGT	M kansasii
4143	, <u>-</u> CMGGM	a[]AAGCC[]G	TAGGGAG <u>IC</u>	gatagg <u>h</u> aa:	ATCCGT	M. smegmatis
		1970	1980	1990	200	0
2908	AGGGGG	ACCGGAATA	TCGTGAACAC	CCTTGCGGT	GGAGC	M.tuberculosis
2208	AGGGGG	CCGGAATA	CCTGAACAC	CCTTGCGGT	GGAGC	M avium
2208	AGGGGGG	CCGGAATA	CCGTGAACAC	CCTTGCGGT	GGAGC	M.paratuberc.
2231	AGGGGGG	CCGGAATA	CGTGAGGGC TCGTGAACAC	:CCTTGCGGGG	GDAGC	M.phlei M.leprae
1910						M gastri
1934	AGGGGGA	CCGGAATA	GCGTGAACAC	ссттессет	GGAGC	M kansasii
4385	AGGGGGF	CCCAGATG	GCGTGMAAGC	CITTACGGCC	CCAAGC	M.smegmatis
		2410	2420	2430	2440	
3345	ACTCGA	1				.tuberculosis
284	ACCTCGA	JGCCAGTTG	GGGCGGAGTC	GTTGTTGAAZ	TEC M	howie
2645	GCACAGA	CGCCAGTTT	GIGIGGAGTO	GTTGTTGAAA	TACC M	.avi:m
393 2645	ATACAGA	CGCCAGTTT	GTATGGAGTC	GTTGTTGAAA	TACC M	.intracellulare
2737	GCTCGGA	CGCCAGTTC	GGGTGGAGTC	GTTGTTGAAA GTTGTTGAAA	TACC M	.paratuberc.
2668	ACTTCGAC	CGCTAGTTG	GGGIGGAGTC	GTTGTTGAAA	TACC M	.leprae
1910	_				M	.gastri
2372	ACCTCAA	CGCCAGTTG	GGGMGGAGTC	CTTCTTCTTCTTT	TOCO M	le composant d

## Figure 1H

2372 ACCTCMACGCCAGTTGGGGTGGAGTCGTTGTTGAAATACC M.kansasii 4822 GCTCACACGCCAGTGTGGGTGGAGTCGTTGTTGAAATACC M.smegmatis

	2450	2460	2470	2480	
2205	7 CTCTTC 7 TTCCTT 7				
324	ACTCTGATCGTATT	GGCATCTAAC	CTCGAACCC'	TGAATC 1	M.tuberculosis
		GGGCATCTAAC	CTCGAACCC	rgaatc 1	M.bovis
433	ACTCTGATCGTATT	GGACACCTAAC	GTCGAACCC:	THATC 1	M.avium
400	ACICIGATOGTATI	GUACACCTAAC	IGM C G A A C C C C	Τ⊫-πίχπι~ κ	A introperty
2003	ACTCTGATCGTATT	GGACACTAAC	GTCGAACCC:	I DIAIC 1	M.paratuberc.
2700	ACTCTGATCGTATT	'GGGCQTCTAAC	CTCGGACCG:	rggatc 1	M.phlei
1910	ACTCTGATTGTATT	'GAACATCTAAC	CTCGAACCG:	MATATC 1	4.leprae
				1	1.gastri
4414	ACTCTGATCGTATT	'GGACACCTAAC	GTCGAACCC:	rgaatc n	1.kansasii
4862	ACTCTGATCGTATT	'GGGC <mark>O</mark> TCTAAC	CTCGGACCG1	PATATC N	1.smegmatis
	2490	2500	2510	0500	
		· · · · · · · · · · · · · · · · · · ·		2520	
3425	GGGTTTAGGGACAG	TGCCTGGCGGG	TAGTTTAACT	rggggc 1	1.tuberculosis
364	GGGTTTAGGGACAG	TGCCTGGCGGG	TAGTTTAACT	rggggc N	1 hovis
2724	GGGTTDADGGACAG	TGCCTGGCGGG	TAGTTTAACI	rggggc N	1.avium
472	GGGTT QA QGGACAG	TGCCTGGCGGG	TAGTTTAACT	reegec N	1 intracellulane
2724	GGGTTICAICIGGACAG	TGCCTGGCGGG	<u>ምልር ምምምል አርባ</u>	reecec N	I nanatukana
28T /	PGGTTPAGGGACAG	TGCCTGGTGGG	TAGTTTAACT	GGGGGC M	1 nhlei
2/48	GGTTTAGGGACAG	TGCCTGGCGGG	TAGTTTAACT	GGGGC M	1.leprae
1910					1 destri
2452	GGGTTGAGGGACAG	TGCCTGGCGGG	TAGTTTAACT	GGGGC M	1 kansasii
4902	GGTTGAGGGACAG	TGCCTGGFGGG'	TAGTTTAACT	GGGGC M	1.smegmatis
					g
	*				
			<del></del>	r	
	2930	2940	2950	2960	)
3864	AGTACGAGAGGACC	GGGACCCACCA	T.CCMCMGGM	202.202	M.tuberculosis
3163	AGTACGAGAGGACC	GGCD CCCD CCD	ACCICI <u>GGT</u>	GOACCA	M.tuberculosis
3163	AGTACCACACCACC	CCCA CCCA CCA	ACCTOTEGT	ATACCA	M.avıum
3256	AGTACGAGAGGACC	CCCA CCCACGA	ACCTUTGGT	ATACCA	M.paratuberc.
3107	AGTACGAGAGGACC	GGGACGACGA	ACCTCTGGT	ATACCA	M.phlei
1910	AGTACGAGAGGACC	GGGACGA	ACCTCTGGT		
	7.007.007.00	_	·		M.gastri
Z891	AGTACGAGAGGACC	GGGACGGACGA	ACCTCTAGT	GCACCA :	M.kansasii
5342	AGTACGAGAGGACC	GGGACGGACGA	ACCTCTGGT	ATACCA	M.smegmatis

# Figure 11

GLASS CHACLASS



		970	2980	2990	300	0
3904		GCAGGGG:	CACCGCTGGA	ATAGCCACGT	СССТ	M.tuberculosis
3203	GTTGTCCC	ACCAGGGG:	CACGGCTGGA	ATAGCCACGT	rcech	M.avium
3203	GTTGTCCC	ACCAGGGG	CACGGCTGG	TAGCCACGT	rcagn	
3296	GTTGTCCC	ACCAGGGG	CACCGCTGG	TAGCCACGT	CGGR	M.paratuberc. M.phlei
3227	GTTGTCTC	ACCAGGGG	CACCGCTGGZ	TAGCCACGT		
1910	)	_			. CGGIA	M.leprae
2931	GTTGTCCC	CCAGGGG	TACCGCTGG	TAGCHACGTI	acce E	M.gastri
5382	GTTGTCCC	CCAGGGG		TAGCEJACG TI	CGGA	M.kansasii
		<u>,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,</u>	roplaciaer	TAGCCACGTT	CGGA	M.smegmatis
		-	<del></del>			
	30	010	3020	3030	3040	)
3944	CAGGATAAC	CGCTGDAD	GCATCTAAC	CCCCTTTCCT		M.tuberculosis
	CAGGATAAC	СССТСАДА	CCATCIAAG	cgggaaacct cgggaaacct	TOTO	M.tuberculosis
3243	CAGGATAAC	CGCTGAAA	CCATCTAAG	CCCCAAACCT	TOTO	M.avium M.paratuberc.
3336	CAGGATAAC	CGCTGAAA		CGGGAAACCT	TCTC	M.paratuberc.
3267		CGCTGAAA		CGGGAAACCT		M.phlei
1910	o. Florrithe	COCIGAAA	GCATCTAAG	CGGGAAACCT		
2971	CAGGATAAG	CCCMCDDD	CCAMOMATA A	~~		M.gastri
5422		CCCCCTATA	GCATCTAAG	CGGGAAACCT	TCTC 1	M.kansasii
0 122	CAUGATAAC	CGCIGAAA	GCATCTAAG	UGGGAAACCT	CTTC I	M.smegmatis
				• =		
	5					
	20	90	2100			
			3100	3110	3120	
4023	CCCGC-AGAI	ACACGGGTT	CAATAGGT C	AGACCTGGAA	GCT M	.tuberculosis
609	CCCGC-AGAI	ACACGGGTT	CAATAGGTC	AGACCTGGAA	GСТ М	.bovis
3322	CCCGC-AGAK	CACGGGA	TGATAGGC	AGACCTGGAA	сст м	.avium
677	CCCGC-AGAK	CACGGGTI	rcgataggdc	AGACCTGGAA	аст м	.intracellulare
3322	CCCGC-AGA	ncacgggan	TIGATAGGIC	AGACCTGGAA	GCT M	.paratuberc.
3415	CCCGC-AGA	CACGGGA	CGATAGAC	agacctg ab		.phlei
3309		J			_	.leprae
1910					M	.gastri
3050	CCCGC-AGA	\CACGGGTT	CGATAGGOC	AGACCTGGAA	эст м	.kansasii
5501	CCCGC-AGA	CACGGGAT	FGATAGAC	AGACCTGGAA	_	.smegmatis
	_				- OM 1/1	· -mcymac15

Figure 1J

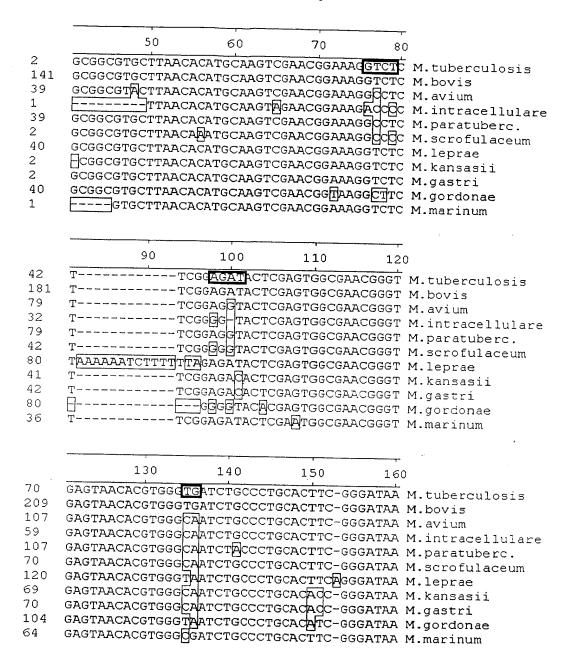


Figure 2A

Tu. Isuaclass



	17	0 18	0 190	20	•
100			- 230	20	~
109	GCCTGGGAAA	CTGGGTCTAA!	Paccggatagg <i>i</i>	ACCACGGGA	M.tuberculosis
248	GCCTGGGAAA	CTGGGTCTAA	FACCGGATAGG <i>I</i>	CCACGGGA	M howie
146	GCCTGGGAAA	CTGGGTCTAA	FACCGGATAGG <i>I</i>	CCTCAAGA	M.avium
98	GCCTGGGAAA	CTGGGTCTAA	PACCGGATAGG	CCTTTAGE	M intracellulana
146	GCCTGGGAAA	$\mathtt{CTGGGTCTAA}$	PACCGGATAGG <i>I</i>	ACCITICIA AIGA	M naratuhera
109	GCCTGGGAAA	CTGGGTCTAAT	FACCGGATAGG <i>F</i>	CCACTIGG	M scrofulacoum
160	GCUTGGGAAA	CTGGGTCTAA	l'accggatagg <i>i</i>	CTTCAAGG	M.leprae
108	GCCTGGGAAA	CTGGGTCTAA	[ACCGGATAGG <i>I</i>	CCACTTGG	M kangagii
109	GCCTGGGAAA	CTGGGTCTAAT	raccggatagg <i>e</i>	CCACTTGG	M dastri
143	GCCTGGGAAA	CTGGGTCTAAT	accg/atagga	CCACAGGA	M gardanas
103	GCCTGGGAAA	CTGGGTCTAA1	ACCGGATAGGA	CCACGGGA	M. mara-
			OOOTIAGE	ADDDOROO	M. Marinum
	21	0 220	230	240	
149	TGCATGTCTT	GTGGTGGAAAG	CGCTTTTAGTGG	TGTGGGAT	M.tuberculosis
288	TGCATGTCTT	GTGGTGGAAAG	CGCTTTAGCGG	TGTGGGAT	M. borrie
186	DGCATGTCTT	Treereerare	CFTTTTFACGG	TO TO GOORT	M. DOVIS
138	CGCATGTCTT	TAGGTGGAAAG	C TITTI ACGG	TG TGGGAT	M.intracellulare
186	CCATGTCTT	TEGEGGAAAG	C TITIOCGG	TGTGGGAT	M.intracellulare M.paratuberc.
149	OGCATGHCTT	ZIGGIGGAAAG	CHITTIFGCGG	TGTAGAAT	M.paratuberc.
200	GCATCGCTTC	TECCECCAAAG		TGTGGGAT	M.scrofulaceum
148	CCATGICITY COMMO	TIGGIGGAAAG	C-TTTTTGCGG	TGCAGGAT	M.leprae
149	GCCATGCCTTC	TGGTGGAAAG	C-TTTTGCGG	TGTGGGAT	M.kansasii
183	CATGOCTTO	JTGGTGGAAAG	C-TTTTGCGG	TGTGGGAT	M.gastri
143	CACATGTCOT	YI'GGTGGAAAG	C-TTTT-GCGG	TGTGGGAT	M.gordonae
143	THOATGTOOT	∍TGGTGGAAAG	E-CTTTECGG	TGTGGGAT	M.marinum
	250	260	270	280	
189			2.0		
	DDDDDDDDDGGG	CTATCAGCTT	GTTGGTGGGGT	GACGGCCT	M.tuberculosis
328	GAGCCCGCGGC	CTATCAGCTT	GTTGGTGGGGT	GACGGCCT	M.bovis
224	GGGCCGCGGG	CTATCAGCTT	GTTGGTGGGGT	GACGGCCT	M.avium
176	elecccecec	CTATCAGCTT	GTTGGTGGGGT	GATGGCCT	M.intracellulare
224	GEGCCGCGC	CTATCAGCTT	GTTGGTGGGGT	GACGGCCT	M.paratuberc
187	GGGCCCGCGGC	CTATCAGCTA	GTTGGTGGGGT	GATIGGCCT	M.scrofulaceum
239	GGGCCCGCGG	CTATCAGCTA	attagtgggt	ACGGCCT	M.leprae
186	GGGCCGCGGC	CTATCAGCTT	GTTGGTGGGGT	FACGGCCT	M.kansasii
187	GGGCCCGCGGC	CTATCAGCTT	GTTGGTGGGGT	SACGGCCT	M.gastri
221	GG-CCCGCGGC	CTATCAGCTT	GTTGGTGGGGT	SATIGGCCT	M.gordonae
181	GGCCCGCGC	CTATCAGCTT	GTTGGTGGGGT	ACGGCCT	M marinum
	_			7.000001	ri.mar riidin



450	460	470	480
AAACCTCTTTCACCA	TCGACGAAGO	TCCGGGTTCT	CTCGG M.tubercul
AAACCTCTTTCACCA	TCGACGAAGO	TCCGGGTTCT	CTCGG M.bovis
AAACCTCTTTCACCA	TCGACGAAGO	TCCGGGTTTT	CTCGG M.avium
AAACCTCTTTCACCA			
AAACCTCTTTCACCA	TCGACGAAGG	TCCGGGTTTT	CTAGG M.paratube
AAACCTCTTTCACCA	TCGACGAAGG		TGTGG M.scrofula
AAACCTCTTTCACCA	TCGACGAAGG	TCHGGGAATT	CTCGG M.leprae
AAACCTCTTTCACCA	TCGACGAAGG	TCCGGGTTCT	CTCGG M.kansasii
AAACCTCTTTCACCA			
AAACCTCTTTCACCA	TCGACGAAGG	rcceeermor	CTCGG M.gordonae
AAACCTCTTTCACCA	TCGACGAAGG	TICGGGTTIT	CTCGG M.marinum

	1130	1140	1150	116	•
1069	TCTCATGTTGCCAGC	CGTAATGG	GGGGACTCGT	GAGAG	M. tuberculosis
1208	TCTCATGTTGCCAGC	CGTAATGGT	GGGGACTCGT	GAGAG	M howis
1104	TCTCATGTTGCCAGC	GGTAATGC	GGGGACTCGT	GAGAG	M. avium
1056	TCTCATGTTGCCAGC	GGTAATGC	GGGGACTCGT	GAGAG	M.intracellulare
T038	TCTCATGTTGCCAGC	GGTAATGCA	GGGGACTCGT	GAGAG	M. paratubero
1064	TCTCATGTTGCCAGC	GGTAATGCC	GGGGACTCGT	GAGAG	M scrofulaceum
1119	TCTCATGTTGCCAGCA	CGTAATGGT	GGGGACTCGT	GAGAG	M lenrae
1066	TCTCATGTTGCCAGC	GGTAATGCC	GGGGACTCGT	GAGAG	M. kansasii
1067	TCTCATGTTGCCAGC	GGTAATGCC	GGGGACTCGT	GAGAG	M.gastri
1100	TCTCATGTTGCCAGC	GGTAATGCC	GGGGACTCGT	GAGAG	M.gordonae
1061	TCTCATGTTGCCAGCA	.CGTAATGGT	GGGGACTCGT	GAGAG	M.marinum

	12	50	1260	1270	1280	
1189	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCCCGAGGTT	AAG M	.tuberculosis
1328	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGCGAGGTT	AAG M	.bovis
1224	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGTAAGGTT	AAG M	.avium
1176	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGCAAGGTT	AAG M	.intracellula
.218	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGTAAGGTT	AAG M	.paratuberc.
184	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGCAAGGTT	AAG M	.scrofulaceum
.239	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGCAAGGTT	AAG M	.leprae
.186	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGCGAGGTT	AAG M	.kansasii
.187	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGCGAGGTT	AAG M	.aastri
1220	CAATGGCCGG	TACAAAGG	GCTGCGATGG	CCGCGAGGTT	AAG M	.gordonae
.181	CAATGGCCGG	TACAAAGG	GCTGCGATG	CCGCGAGGTT	AAG M	.marinum



	1290	1300	1310	1320
1229	CGAATCCTTA-A	AAGCCGGTCTCAC	TTCGGATCG	GGTCT M.tuberculosi
1368	CGAATCCTTA-A	AAGCCGGTCTCA	TTCGGATCG	GGTCT M.bovis
1264	CGAATCCTTTTA	AAGCCGGACTCA	TTCGGATTG	GGTCT M.avium
1216	CGAATCCTTTTA	AAGCCGGTCTCA	TTCGGATTG	GGTCT M.intracellul
1258	CGAATCCTTTTA	AAGCCGGACTCAG	TTCGGATHG	GGTCT M. paratuberc
1224	CGAATCCTTTTA	AAGCCGGTCTCAG	TTCGGATCG	GGTCT M. scrofulace:
1279	CGAATCCTTTTA	AAGCCGGTCTCAG	STTCGGATCG	GGTCT M.leprae
1226	CGAATCCTTTTA	AAGCCGGTCTCAG	TTCGGATCG	GGTCT M.kansasii
1227	CGAATCCTTTTA	AAGCCGGTCTCAG	TTCGGATCG	GGTCT M.gastri
1260	CGAATCCTTTTA	AAGCCGGTCTCAG	TTCGGATCG	GGTCT M.gordonae
1221	CGAATCCTTI-A	AAGCCGGTCTCAG	TTCGGATCGC	GGTCT M.marinum
	1330	1340	1350	1360
1268	GCAACTCGACCC	GEGAAGTCGGAG	TCGCTAGTA	TCGCA M.tuberculosi
1407	GCAACTCGACCC	CGTGAAGTCGGAG	TCGCTAGTA	TCGCA M.bovis
1304	GCAACTCGACCC	CATGAAGTCGGAG	TCGCTAGTA	TCGCA M.avium
1256	GCAACTCGACCC	CATGAAGTCGGAG	TCGCTAGTA	TCGCA M.intracellul
1298	GCAACTAGACCC	AATGAAGTCGGAG	TCGCTAGTA	TCGCA M.paratuberc.
1264	GCAACTCGACCC	 CGTGAAGTCGGAG	TCGCTAGTA	TCGCA M.scrofulaceu
1319	GCAACTCGACCC	CGTGAAGTCGGAG	TCGCTAGTA	TCGCA M.leprae
1266	GCAACTCGACCC	CGTGAAGTCGGAG	TCGCTAGTA	TCGCA M.kansasii
1266	GCAACTCGACCC	CGTGAAGTCGGAG CGTGAAGTCGGAG	TCGCTAGTAA TCGCTAGTAA	TCGCA M.kansasii TCGCA M.gastri
1266 1267	GCAACTCGACCC	CGTGAAGTCGGAG	TCGCTAGTAA	TCGCA M.kansasii TCGCA M.gastri TCGCA M.gordonae

Figure 2D

	50	60	70	80	
128 39 41 3559 5743	TTCCGAACCCGGAI TGCCGAACCCGGAI TCCCGAACCCGGAI TACCGAACCCGGAI	AGCTAAGCCTGC AGCTAAGCCTGG AGCTAAGCCTGFF	CAGCGCCGA: CAGCGCCAA: CAGCGCCGA:	TGATAC TGATAC	M.phlei
	90	100	110	120	)
168 79 81 3599 5782	TGCCCTCCGGG-TGCCCTCACGGGG-TGCCCATTCGGG-TACCGGGGGGGGGG	TGGAAAAGT: TGGAAAAGT: TGGAAAAGT:	agg@caccg@ aggacaccg@ aggacac∏g@	CCGAAC CCGAAC	M.phlei

Figure 3



		90	100	110	120	
382	GGGAGCT	GTCAACCGA	GCATTGATCCG.	AGGATTTCCC	777 14	<b></b>
382	GGGAGCT	GTCAACCGA	GCATTGATCCG	AGGATTICCG AGGATTTCCC	AAT M	.avium .paratuberc.
1053	GGGAGCT	GTCAACCGA	SCATEGATOCG	AGGATTICCG AGGATTTTCCG	AAT M	<pre>.paratuberctuberculosis</pre>
467	GGGAGCT	GTCAACCGA	GCGTGGATCCG	AGGATTICCG	AAT M	tuberculosis
392	GGGAGCT	GTCAACCGA	GCGTGGATCCG:	AGGATT TCCG	AAT M	.pnle1
167	GGGAGCT	TCAACCGA	SCGTGGATCCG:	AGGATTTCCG AGGATTTCCG	AAT M	.leprae
110	GGGAGCT	TCAACCGA	SCGTGGATCCG	AGGAI TTCCG	AAT M	.gastri
2548	GGGAGCT	TCDDCCCAC	GCGTTGATCCG	AGGATTTCCG	AAT M	.Kansasii
	0007.001	JI OAROOGA	30011GATCCG/	AGGATETICCG	аат м	.smegmatis
			,	<b>-</b>		
		170	180	190		
1.00	~~~~				200	
462	GAATATAT	TAGGGTGCG-	GGAGGTAACGG	CGGGGAAGTG	M AAA	.avium
462	GAATATAT	AGGGTGCG-	-GGAGGTAACG0	CGGGGAAGTG:	AAA M	.paratuberc.
1133 547	GAATATAT	'AGGGTGCG-	GGAGGGAACG	CGGGGAAGTG	AAA M.	tuberculosis
472	GAATATAT	'AGGCGTTG-	GGGGGAACGC	CGGGGAAGTG	AAA M.	.phlei
247	GAATATAT	AGGGTECG-	GGAGGGAACGC	GGGGAAGTG	AAA M.	.leprae
190	GAATATAT	'AGGGTGCG-	GGAGGGAACGC	GGGGAAGTG	AAA'M.	gastri
	GAATATAT	'AGGG'I'GCG-	GGAGGGAACGC	GGGGAAGTG	AAA M.	kansasii
2020	GAATATAT	.Aeece.lcII-	GGGGGAACGC	GGGGAAGTG	AAA M.	smegmatis
				•		
		250	260		т-	
				270	280	
541·	-GTCAGTA	GTGGCGAGC	GAAC-CGGAAC	A-GGCTAAAC	CG M.	avium
541	-GTCAGTA	GTGGCGAGC	GAAC-CGGAAC	A-GGCTAAAC	CG M	naratubero
1212	-GCAAGTA	GTGGCGAGC	GAACGCGGAAC	$\Delta - GGCTDDDD$	CC M	tuborquilogia
040	-GTGAGTA	GTGGCGAGC	GDDH DAGGDRA	אואוכככיייא א א כ	CC 14	-1-1-3
551	-GCAAGTA	GTGGCGAGC	GAACGTGGAAN GAACGCGGAAC	ANGGCTAAAC	CG M.	leprae
326	-GTCAGTA	GTGGCGAGC	GAACGCGGAAC	AIGGCTAAAC	CG M	gastri
209	-GIPAGTA	GTGGCGAGC	GAACIGCGGAAC.	AIIGGCTAAAC	CG M.	kansasii
2706	ggtgagta:	GTGGCGAGC	GAACACGGAGG	ANGGCTAAAC	FG м.	smegmatis
				_	_	3

Figure 4A

DRAF 13



	<del></del>	····		~		
		290	300	310	320	
578 578 1250 664 590 365 308 2745	CATG-CATG-CATG-CATG-CATG-CATG-CATG-CATG-	ATGGACAACO ATGGGTAACO ATGTCATAACI ATGGGTGACO ATGGGTAACO	GGGTAGGGG GGGTAGGGG GGGTAGGGG GGGTAGGGG GGGTAGGGG	TTGTGTGTGC TTGTGTGTGC TTGTGTGTGC TTGTGTGTG	GGGGT GGGGT GGGGT GGGGT GGGGT	M.avium M.paratuberc. M.tuberculosis M.phlei M.leprae M.gastri M.kansasii M.smegmatis
		330	340	350	360	
617 617 1289 703 629 404 347 2785	TGTGGGA TGTGGGA TGTGGGA TGTGGGA TGTGGGA	ATTGATATGT AG-GATATGT ECCTGTGTGT ATTGGTATGT ATGGATAGGT ATGGATAGGT	CTCAGCTCT CTCAGCGCT CTCAACTCT CTCAGCTCT CTCAGCTCT CTCAGCTCT	ACCTGGCTGA ACCTGGCTGA ACCCGGCCGAT ACCTGGTTGA ACCCGGCTGA ACCCGGCTGA ACCCGGCTGA	GG-GG GG-GG GA-GG GG-GG GG-GG GG-GG	M.avium M.paratuberc. M.tuberculosis M.phlei M.leprae M.gastri M.kansasii M.smegmatis
		370	380	390	400	
742 668 443 386	TAGTCAG  CAGTCAG  TAGTCAG  TAGTCAG  CAGTCAG  CAGTCAG	AAAGTGTCG AAAGTGTCG AAAGTAGTG AAAGTGCG AAAGTGTCG AAAGTGTCG	IGGTTAGCG( IGGTTAGCG( IGGTTAGCG( IGGTTAACGC	SAAGTGGCCTO	GGAC 1 GGGAT 1 GGGAT 1 GGGAT 1 GGGAT 1 GGGAT 1	M.avium M.paratuberc. M.tuberculosis M.phlei M.leprae M.gastri M.kansasii M.smegmatis

# Figure 4B

		410	420	430	440
696 696 136 782 708 483 426 286	GOTOTO GOTOTO GOTOTO GOTOTO GOTOTO GOTOTO	CCGTAGACG CCGTAGTGG CCGTAGACG CCGTAGACG	GTGAGAGCCC GTGAGAGCCC GTGAGAGCCC GTGAGAGCCC	CGGTACGCGAA CGTACGCGAA CGTACGCGAA CGGTACGTGAA	A-ACC M.avium A-ACC M.paratuberc.
		450	460	470	480
735 735 1406 820 747 522 465 2902	CGGCACO TGCTGCO TGGCACO CGGCACO CGGCACO	TGCCTAGTA GCTGTCAC TGCCTTGTA TGCCTTGTA	TCAAFTCCCC AGGTCCCC TCAAFTCCCC	JAGTAGCAGCG JAGTAGCAGCG JAGTAGCAGCG JAGTAGCAGCG	GGCC M.avium GGCC M.paratuberc. GGCC M.tuberculosis GGCC M.phlei GGCC M.leprae GGCC M.gastri GGCC M.kansasii GGCC M.smegmatis
				<b>-</b> -	
855 855 1526 937 867 642 585 3022	GAGGGAAT GAGGGAAT GAGGGAAT GAGGGAAT	rggtgaaaag Ggtgaaaag Ggtgaaaag 'Ggtgaaaag	TACCCCGGG TACCCCGGG TACCCCGGG TACCCCGGG	AGGGAGTGAA AGGG-AGTGAA AGGGGAGTGAA AGGGGAGTGAA	600  ATA M.avium  ATA M.paratuberc.  AGA M.tuberculosis  AGA M.phlei  ATA M.leprae  AGA M.gastri  AGA M.kansasii  AGA M.smegmatis

Figure 4C

...FIG. Tags paudicass

		610	620	630	640	)
894 894 1566 976 907 682 625 3062	GTACCTG GTACCTG GTACCTG GTACCTG	AAACCGTGT AAACCGTGT AAACCGTGT AAACCGTGT	GCCTACAAT GCCTACAAT GCCTACAAT GCCTACAAT	CCGTCAGAG CCGTCAGAG CCGTCAGAG	COTCCT CCTCCT CCTCT CCTCTT CCCCTTT	M.avium M.paratuberc. M.tuberculosis
024	·	650	660	670	680	
947 722 665	C CTTCCTC CTI I C CCTI CCTI	rccggagga gta (	G 16666 1GAN GGGGGTGAN GTGGGGTGAN GTGGGGTGAN GTGGGGTGAN	GGCGTGCCT GGCGTGCTT GGCGTGCCT GGCGTGCCT	TTTGA 1 TTTGA 1 TTTGA 1 TTTGA 1 TTTGA 1 TTTGA 1	M.paratuberc. M.tuberculosis M.phlei
		590	700	710	720	
959 A 1646 A 4 A 1046 A 972 A 747 A 690 A	GAATGAG( GAATGAG( GAATGAG( GAATGAG( GAATGAG( GAATGAG( GAATGAG( GAATGAG(	CCTGCGAGTO CCTGCGAGTO CCTGCGAGTO CCTGCGAGTO CCTGCGAGTO CCTGCGAGTO	CAGGGACACG CAGGGACATG CAGGGACATG CAGGGACATG CAGGGACATG CAGGGACATG CAGGGACATG	TCGCGAGGT' TCGCGAGGT' TCGCAAGGT' TCGCGAGGT' TCGCGAGGT' TCGCGAGGT' TCGCGAGGT' TCGCGAGGT' TCGCGAGGT'	TAAC M.	intracellulare paratuberc. tuberculosis bovis phlei leprae gastri

Figure 4D

770 780 790 800	
CGCATCCCCTTTGGGGTGTAGTGGCGTGT M  1039 CGCATCCCTTTGGGGTGTAGTGGCGTGT M  1039 CGCATCCCTTTTGGGGTGTAGTGGCGTGT M  1726 CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT M  84 CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT M  1126 CGTATCCAACCTGTTGGGGTTCGTGTAGTGGCGTGT M  1052 CGTATCACGTGTGAGCGTGTGTAGTGGCGTGT M  827 CGTATCACGCGTAAGCGTGTGTAGTGGCGTGT M  770 CGTATCGCGCGCGAGCGTGTGTAGTGGCGTGT M  3212 CGTATCCACACAAGAGTGTGTGGTGTAGTGGCGTGT M	M.intracellulare M.paratuberc. M.tuberculosis M.bovis M.phlei M.leprae M.gastri

	4 4		•	- 1	
	1050	1060	1070	1086	<b>)</b>
1307	CAGCCAAACTCCGAA	ATGCCG-TGGT	G-TDDDDDCC	70000	
2005	CAGCCAAACTCCGAA	TGCCG-TGGT	G-TAAAAGCC	FTGGCA	M.paratuberc.
1401	CAGCCAAACTCCGAA	ALCCCCMMP TO	G-TALIAAGCG	TGGCA	M.tuberculosis
1323	CAGCCALACTCCCA	TGCCGATAAG	- -TGAAAGIIG	TGGCA	M.phlei
1041	CAGCCAAACTCCGAA	VIGCCG-TGGT	G-TAMA-GCG	TGGCA	M.gastri
2400	CAGCCAAACTCCGAA	TGCCGGTAAG	SCOAAGAGIIG	OGGAD 1	M smeamatic
				⊡,- ~ <i>L</i> • • •	· · · · · · · · · · · · · · · · · · ·

	1170	1180	1190	1200
2122 1519 1441 1215 1158	AGTGGAAAAGGATGTC AGTGGAAAAGGATGTC AGTGGGAAAGGATGTC	TAGTCGCAG TAGTCGCAG TAGTCGCAG TAGTCGCAG TAGTCGCAG TAGTCGCAG	A-GACAACCAGG BA-GACAACCAGG A-GACAACCAGG BAGGACAACCAGG B-GACAACCAGG	GAGG M.paratuberc. GAGG M.tuberculosis GAGG M.phlei GAGG M.leprae

# Figure 4E

		50	1260	1270	1280	
1504	CTCACTGGT	CAAGTGA	TTATGCGCCG	ATAATGTAGC	EGGG M	
		. A A   - 1   - A '	ייייטיתכככככסי	N 70 75 75 75 75 75 75 75 75 75 75 75 75 75		avium
		** ** ** * * * * * * * * * * * * * * *	"""""""""""""""""""""""""""""""""""""""	* CT 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	•	paratuberc.
¥000	- O T OMO T G G J (	AAGTGD	PTPC CCCCMC7	\		uberculosis
	O T ONG I G	. A A 1 + 1 1 + A 1	"""""""""""""""""""""""""""""""""""""""	(MX * m	•	hlei
	CICHCIGGIC	AAGTGA1	<sup>ֈ</sup> ͲϏͲϾϹϾϹϹͼϭ	TIN A MARKET		eprae
1201	OTCHCIGGTC	:AAGTGA1	יידוקודופרפרכיי	TIND TO COME OF A COME		astri
3686	TCACTGGTC	AAGTGAT	TGTGCGCCG	TATTETECC	CCC M. K	ansasii
					GGG M.S	megmatis
	129	90	1300	1210	<del></del>	
1544	COCAACCA			1310	1320	
1544	CTCAAGCACA	CCGCCGA	AGCCGCGGCA	CATTCATCTT	TA M.a	vium
~ 0 1 1	CICARGUACA	UUGUUGA	AGCCGCCC			aratuhero
						uberculosis
	CICHUACACA	JUGUUGA	AGCCCCC $C$	700000000000000000000000000000000000000	_1_1.1	
-000	OLCHURCHUR	JUGUUGA	AGCCGCGCCM	CATTCACCTT	TA M. 1	aprae
			はこうしい いいしいひかん	AddGd	FA M.a.	astri
	CTCAAGCACA	CCGCCGA	agccgcgaca		1	ansasii
3720	TCAAGCACA	CCGCCGA	AGCCGCGGAA	GCAACGT		megmatis
						egac13
_						
	133	^	1 2 4 2		<del></del>	
1500 =		-		1350	1360	
1583	GGTGGATGTG	GGTAGGG	GAGCGTCCCC	CATTCAGCGE	AG M as	(i 11m
_		OG I MUTUTO	1 - 41 - 1 - 1 - 1 - 1 - 1 - 1	CD $DD$ $DD$ $DD$ $D$ $D$ $D$ $D$ $D$ $D$		
	O TOOKIGIG	GGTWGGG	GAGCGTINCCIT	CATTCAGCGA	AC M 10	<b></b>
1		OGIMGGG	GAGUGTCCCT	CATTCAGCGA	AC M ~ a	material district
	110	GGTAGGG	GAGCGTCCCM	CD $T$	70.01 1.	
3764 T	TTG	GGTAGGG	GAGCGTCCTG	-atecega -atecegeiga	no M.Ka	1124211
				· • ⊠~⊠~⊞G¥	ug M.SIII	eymatis

Figure 4F

* * * * * * * * * * * * * * * * * * * *				
1.50.0	1370	1380	1390	1400
1402 CCGCCC	GGTGACCGG GGGTGA[[CGG GGGTACCGGG GGGTGACCGG	TGGTGGAGG TGGTGGAGGG TGGTGGAGGG TGGTGGAGGF	FTGGGGGAGTG FTGGGGGAGTG FTGGGGAGTG FTGGGGGAGTG	AGAAT M.paratuberc. AGAAT M.tuberculosis
			<b></b>	
<del></del>				
	1530	1540	1550	1560
1875 CGATGG 1800 CGATGG 1562 CGATGG 1505 CGATGG	ACAACGGGTT ACAACGGGTT ACAACGGGTT ACAACGGGTT ACAACGGGTT ACAACGGGTT	GATATTCCC GATATTCCC GATATTCCC GATATTCCC GATATTCCC	STACCCGTGT/ STACCCGTGT/ STACCCGTGT/ STACCCGTGT/ STACCCGTGTC	ATGGG M.avium ATGGG M.paratuberc. TGGG M.tuberculosis ATGAG M.phlei TGIG M.leprae TGGG M.gastri TGGG M.kansasii TGIG M.smegmatis
2519 CGGCCGT 1915 CGTCCCT 1840 CGGCCGT 1602 CGCCCGT 1545 CGCCCGT	GAGGAATCA- GATGAATCFC GATGAATCA- GATGAATCA- GATGAATCA-	GCGGTACTA GCGGTACTA GCGGTACTA GCGGTACTA	ACCACCCAA ACCACCCAAA ACCACCCAAA ACCACCCAAA ACCACC	1600 ACCG M.avium ACCG M.paratuberc. ACCG M.tuberculosis ACCI M.phlei ACCG M.leprae ACCG M.gastri ACCG M.kansasii ACCA M.smegmatis

# Figure 4G

		1610	1620	1630	4.4.	
186	O GAT	-CGICCAT-T	TCCCCTTTC		1640 TT-CEG M.avium	
186	O GAT	-CGACCAT-T		C-GTGGCGA	TT-CGG M.avium TT-CGG M.paratuber	
255	8 620	-canfficaff-m	000000	ASSESSED A	TT-CGG M.paratuber	c.
195	5 GG d	-CGAMCE-AIT	CCmmcaaaa	1 -10 - 6-6-1-10-1	TUTIGG M.tuberculo	sis
187	9 GAT	-CGACCATAT		T G T GHC G G	TTG-GG M.phlei	
164	1 GAT-	-CGAMCAME	CCCCEEC	ATT GOLIGIA	TT-CGG M.leprae	
158	4 GAT-	-CGATCAC-T	CCCCTTCGGGG	C-CTCCDCC	TC-TGG M.gastri TC-TGG M.kansasii	
403	5 ACC	FIGACCECAC	CTTTCGGGG	-TCTCCCC	TC-TGG M.kansasii TGGTGG M.smegmatis	
					1GG1GG M.smegmatis	
		1650	1.000		<del></del>	
100			1660	1670	1680	
1896	GGCI	'GCGTGGGACC	CTTCGCTGGTAG	TAGTCAAGG	ATGG M.avium	
7090	9 GGCT	GCGTGGGACC	CTTCGCTGGTAG	TAGTCAAGC	MTGGG M.avium NATGGG M.paratubero	~
1000	GGCT	GCGTGGGAAC	CTTCGCTGGTAG	TAGTCAAGC	ATGGG M.paratuberd	
1017	GGCT	GCGTGGGACC	CG-GTGGGTAG	TAGTCAAGC	AAGGG M.tuberculos ATGGG M.phlei	172
1677	CCCM	GCGTGGGAAC	TTCGITGGTAG'	TAGTCAAGC	ATGGG M.phlei ATGGG M.leprae	
1620	CCC	GCGTGGAGCC	TTCGCTGGTAG	TAGTCAAGCG	ATGGG M.leprae ATGGG M.gastri	
4071	. 6661	GCATGGGACC	TTCGTTGGTAGT	ragtcaagc	ATGGG M.kansasii ATGGG M.smegmatis	
				_	- J	
			-			
		1690	1700	1710	1720	
1936	-GTG	CGCAGGAAG	GCAGCCGTACCA			
1936	-GTG	CGCAGGAAG	GCAGCCGTACCA GCAGCCGTACCA	GTCAGTGGT	AATA- M.avium AATA- M.paratuberc	
2634	-GTG	CGCAGGAAG	GMAGCCGTACCA	GTCAGTGGT	AATA- M.paratuberc AACA- M.tuberculos	•
2025	-GTGA	CGCAGGAAG	GIAGCCGTACCA	GTCDCTGGT	AAQA- M.tuberculos AATA- M.phlei	is
4111	-GTGA	CGCAGGAAGG	FRAGCCGTACCE	OT CAGIGGIY GTCAGTCCTT	AATA- M.kansasii AATA- M.smegmatis	
			- G	OI CAGIGGTA	MATA- M.smegmatis	
		1720			<del></del>	
		1730	1740	1750	1760	
19/4	-CTGG	GGCAAGCCCG	TAGAGAGCG	ATAGGCAAAT	CCGT M.avium	
40 <i>12</i>	-CTGG	GGCAAGCCGG	TAGGGAGAGCG	ATAGGCAAAT	CCGT M.paratuberc. CCGT M.tuberculosi	· i ~
4063 1005	-CUGG		TAGGGGGAGTG	ATAGGCAAAT	CCGT M.tuberculosi CCGT M.phlei	. 3
1600	-CTGG	GCAAGCCAG	TAGGGAGAGCGA	TAGGCAAAT	CCGT M.leprae CCGT M.gastri	
1149	-chaga	JG[]AAGCC[]G	TAGGGAGTCAG	TAGGTAAAT	CCGT M.kansasii CCGT M.smegmatis	
				J	21110 31110 513	

# Figure 4H

		1810	1820	1830	184	In
205	51 CG-2	AATTCGGTGA	PCCTCTGCTGC			
275	1 CG-2	AATTCGGTGAT	CCTCTGCTGC	CAAGAAAAGC	CICIA-	M.paratuberc. M.tuberculosis
214	1 CG-2	ATTCGGT <u>G</u> AT	CCTATGCTG	CGAGAAAAGC	CTC1M-	M. tuberculosis
183	4 CG-7	ATTCGGTGAT	CCTCTGCTGC; CCTCTGCTGC	CAAGAAAAGC	CTCTA-	M. Teprae
1//	/ CG-F	ATTCGGTGAI	CCTCTGCTGC	CAAGAAAAGC	CTCTA-	M.kansasii
422	8 CG-F	ATTCGGTGAT	CCTATGCTGC	GAGAAAAGC	CTCTA-	M.kansasii M.smegmatis
				_		r. smegmatis
		1850	1860	1870	1880	)
2089		GCACATACAC	GCCCGTACCC	CADACCAACT		
2089		JOHON L MOMOL	UGCCCGTACCC	<b>ペカルカペペッカペッ</b>	~~~	M.avium
2789	~~~~~	JUNUALIALI		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		M.paratuberc.
2179		JUDICATALALI	HACCCCTTA CCC	~~~~~~		M.tuberculosis M.phlei
		2 CHITAMANITACE	iGCCCCTTTCCC	ペカカカペートー ーー		M.leprae
		JUAUAUAU AL I		~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		M.gastri
1010	CCGAC	CACACIACIACI	GCCCCCC CCC	77 7 7 7 ~ - -		gustri 1.kansasii
4200	GCGAG	GACATACACG	GCCCGTACCC	CAAACCĀACA		1.smegmatis
				<del>-</del> -		
					<del></del>	
	·	1970	1980	1990	2000	
2208	AGGGG	CCCGGAATA	CCGTGAACACC	CTTGCGGTG	GREC N	.avium
2208	AGGGG	GCCCGGAATA	ここにはしませんかんしん	Commanda		
2908						.paratuberc. .tuberculosis
						.phlei
2231	AGGGG	GGCCGGAATA[	CGTGAACACC	CTTGCGGTGG		.leprae
1910 1934						
4385	AGGGG	JACCGGAATAC	CCTGAACACC	CTTGCGGTGG		.kansasii
4303	DUUUH	HCCCAGATGO	CGTGTAAGCC	TTECGCCC	AAGC M	.smegmatis
						<b>J</b> – <b>-</b>
			<del></del>			
		2010	2020	2030	2040	
2248	GGGAT	CGGCCGCAGE	AACCACEC	77777		
2248	GGGATT	CGGCCGCAGA	AACCAGTGGG	TAGCGACT-G	TTTA M	.avium .paratuberc.
2948	GGGAT	CGGTCGCAGA	AACCAGIGGG	TAGUGAUT-G	TTTA M	.paratuberc. .tuberculosis
2338	GGGGT	GGGTGGCAGA	AACCAGTGAG AACCAGTGAG GACCAGTGAG	SAGCGACT-G	TTTA M	tuberculosis
2271	GGGAT	CGGTCGCAGA	GACCAGTGAG	PAGCGACT-G	M ATTT	.pnlei
1910		_		AVOCANCI - G	TITA M	.leprae
1974	GGGATT	'CGGTTCGCAGA	AACCAGTGAGA	AGCG A CTMC		gastri
4425	GIIGAGI	GGGTGGCAGA	AACCAGTGAG	AGCGACTEG	יא עידיד. דיד אינערייי	. Kansasii
			٠٠٠٠	7 001101 G	TILA M.	smegmatls

Figure 41

		130	2140	2150	210	- 50
3067 2457 2390 1910 2094	CCGTTAACC CIGTTAACC	CGG-AA	GGGTGAAGC GGGTGAAGC GGGTGAAGC	GGAGAATTTA GGAGAATTTA GGAGAATTTA	AGCCC AGCCC AGCCC AGCCC	M.paratuberc. M.tuberculosis
						J
		50	2260	2270	228	0
3185	GTAACGACT	rcffcaac	rGTCTCAAC( rgmcmcnncc		CGAA	M.paratuberc.
2508 1910	GTAACGACTI	rciicaac:	GTCTCAACC	ATAGACTEGO ATAGACTEGO	CGAA CGAA	M.phlei M.leprae
4663	GTAACGACTI	CICAACI	GTCTCAACC	ATAGACTCGG ATAGACTCGG	CGAA CGAA	M.gastri M.kansasii M.smegmatis
0.55-	23	-	2380	2390	2400	)
3305 2697 2628 1910	GTTCGGTACG GTTCGATACG GTTCGGTGCG	GTTTGTG GTTTGTG GTTTGTG	TAGGATAGG' TAGGATAGG' TAGGATAGG' TAGGATAGG'	I'GGGAGACTG' I'GGGAGACTG' I'GGGAGACTG'	TGAA 1 TGAA 1 TGAA 1 TGAA 1	M.paratuberc. M.tuberculosis M.phlei M.leprae
	GOTCGATACG	GTTTGTG' GTTTGTG'	PAGGATAGG PAGGATAGG	rgggagactg rgggagactg		4.kansasii 4.smegmatis

Figure 4J

```
2410
                         2420
                                    2430
                                               2440
 2645 GCACABACGCCAGTTTGTGTGGAGTCGTTGTTGAAATACC M.avium
      ATACAGACGCCAGTTTGTATGGAGTCGTTGTTGAAATACC M.intracellulare
 2645 GCACAGACGCCAGTTTGTGTGGAGTCGTTGTTGAAATACC M.paratuberc.
 3345 ACCTGGACGCCAGTTGGGGGGGAGTCGTTGTTGAAATACC M.tuberculosis
284 ACCTGGACGCCAGTTGGGGGGAGTCGTTGTTGAAATACC M.bovis
2737 GCTGGGACGCCAGTTGGGGGGGGGGGGGGGTCGTTGTTGAAATACC M.phlei
2668 Acttdgacgcffagttggggtggagtcgttgttgaaatacc m.leprae
1910
2372 ACCTCAACGCCAGTTGGGGTGGAGTCGTTGTTGAAATACC M.kansasii
4822 GCTCACACCCAGTCTGCGTGGAGTCGTTGTTGAAATACC M.smegmatis
              2450
                         2460
                                    2470
                                               2480
 2685 ACTCTGATCGTATTGGACACCTAACGTCGAACCCT-TATC M.avium
 433 ACTCTGATCGTATTGGACACCTAACGTCGAACCCT-TATC M.intracellulare
2685 ACTCTGATCGTATTGGACACCTAACGTCGAACCCT-TATC M.paratuberc.
3385 ACTCTGATCGTATTGGGCATCTAACCTCGAACCCTGAATC M.tuberculosis
324 ACTCTGATCGTATTGGGCATCTAACCTCGAACCCTGAATC M.bovis
2777 ACTCTGATCGTATTGGGCCTCTAACCTCGGACCGTGGATC M.phlei
2708 ACTCTGATIGTATTGACAICTAACCTCGAACCGTATATC M.leprae
1910
2412 ACTCTGATCGTATTGGACACCTAACGTCGAACCCTGAATC M.kansasii
4862 ACTCTGATCGTATTGGGCCTCTAACGTCGGACCGTATATC M.smegmatis
              2690
                         2700
                                     2710
                                                2720
2924 GGTGTCACTCAACGGATAAAAGGTACCCCGGGGATAACGG M.avium
2924 GGTGTCACTCAACGGATAAAAGGTACCCCGGGGATAACAG M.paratuberc.
3625 GGTGTCGCTCAACGGATAAAAGGTACCCCGGGGATAACAG M.tuberculosis
3017 GGTGTCGCTCAACGGATAAAAGGTACCCCGGGGATAACAG M.phlei
2948 GGTGTCGCTCAACGGATAAAAGGTACCCCGGGGATAACAG M.leprae
                                                    M.qastri
2652 GGTGTCGCTCAACGGATAAAAGGTACCCCGGGGATAACAG M.kansasii
5102 GGTGTCGCTCAACGGATAAAAGGTACCCCGGGGATAACAG M.smegmatis
              2730
                         2740
                                     2750
                                                2760
2964 GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG M.avium
2964 GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG M.paratuberc.
3665 GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG M.tuberculosis
3057 GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG M.phlei
2988 GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG M.leprae
2692 GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG M.kansasii
5142 GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG M.smegmatis
```

Figure 4K

```
2770
                         2780
                                    2790
                                               2800
 3004 GCACCTCGATGTCGGCTCGCATCCTGGGGCTGGAGCA M.avium
 3004 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.paratuberc.
 3705 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.tuberculosis
 3097 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.phlei
3028 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGAAGCA M.leprae
2732 GCACCTCGATGTCGGCTCGCATCCTGGGGCTGGAGCA M.kansasii
5182 GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA M.smegmatis
              2810
                         2820
                                    2830
                                              2840
3044 GGTCCCAAAGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.avium
3044 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.paratuberc.
3745 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.tuberculosis
3137 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.phlei
3068 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.leprae
1910
2772 GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAAGCGGCAC M.kansasii
5222 GGTCCCAAGGGTTGGGCTGTTCGCCCGATTAAAGCGGCAC M.smegmatis
             3050
                        3060
                                   3070
                                             3080
3283 CAAGATCAGGTTT-CTCACCCTTTTAGAGGGATAAGGCCC M.avium
638 CAAGATCAGGTTT-CTCACCCTTTTAGAGGGGATAAGGCCC M.intracellulare
3283 CAAGATCAGGTTT-CTCACCCTTTTAGAGGGGATAAGGCCC M.paratuberc.
3984 CAAGATCAGGTTT-CTCACCCACTTGGTGGGATAAGGCCC M.tuberculosis
570 CAAGATCAGGTTT-CTCACCCACTTGGTGGGATAAGGCCC M.bovis
3376 CAAGADCAGGOTT-CTCACCCTDTACGAGGGATAAGGCCC M.phlei
3307 CAA
                                                 M.leprae
1910
3011 CAAGATCAGGGTT-CTCACCCAGTTGGTGGGATAAGGCCC M.kansasii
5462 CAAGACCAGGCTT-CTCACCCTCTAGGAGGGATAAGGCCC M.smegmatis
             3090
                        3100
                                   3110
                                             3120
3322 CCCGC-AGACCACGGGATTGATAGGCCAGACCTGGAAGCT M.avium
677 CCCGC-AGACCACGGGTTGGATAGGCCAGACCTGGAAGCT M.intracellulare
3322 CCCGC-AGATCACGGGATTGATAGGCCAGACCTGGAAGCT M.paratuberc.
4023 CCCGC-AGAACACGGGTTCAATAGGTCAGACCTGGAAGCT M.tuberculosis
609 CCCGC-AGAACACGGGTTCAATAGGTCAGACCTGGAAGCT M.bovis
3415 CCCGC-AGACCACGGGATGGATAGACCAGACCTGGAGGCA M.phlei
3309
                                                 M.leprae
1910
                                                 M.gastri
3050 CCCGC-AGAACACGGGTTGGATAGGCCAGACCTGGAAGCT M.kansasii
5501 CCCGC-AGACCACGGGATTGATAGACCAGACCTGGAAGC M.smegmatis
```

#### Figure 4L

		130	140	150	160	
107 59 107 76 70 209 120 69 70 104	GAGTAACA	CGTGGGCAI CGTGGGCAI CGTGGGTGI CGTGGGTGI CGTGGGTAI CGTGGGCAI CGTGGGCAI CGTGGGCAI CGTGGGCAI	ATCTGCCTG ATCTGCCTG ATCTGCCCTG ATCTGCCCTG ATCTGCCCTG ATCTGCCCTG ATCTGCCCTG ATCTGCCCTG ATCTGCCCTG	CACTTC-GGGA CACTTC-GGGA CACTTC-GGGA CACTTC-GGGA CACTTC-GGGA CACTTC-GGGA CACTTCAGGGA CACTCAGGGA CACACC-GGGA CACACC-GGGA CACATC-GGGA CACATC-GGGA	TAA M.ir TAA M.pa TAA M.so TAA M.tu TAA M.bo TAA M.le TAA M.le TAA M.ka	ntracellulare eratuberc. crofulaceum uberculosis ovis eprae ensasii
		150	460	470	480	
424 376 424 387 389 528 439 386 387 420 381	AAACCTCTT AAACCTCTT AAACCTCTT AAACCTCTT AAACCTCTT AAACCTCTT AAACCTCTT AAACCTCTT AAACCTCTT	TCACCATC TCACCATC TCACCATC TCACCATC TCACCATC TCACCATC TCACCATC TCACCATC	GACGAAGGT GACGAAGGT GACGAAGGT GACGAAGGT GACGAAGGT GACGAAGGT GACGAAGGT GACGAAGGT GACGAAGGT	CCGGGTTTTDT CCGGGTTTTCT CCGGGTTTTCT CCACTTTG CCGGGTTCTCT CCGGGTTCTCT CCGGGTTCTCT CCGGGTTCTCT CCGGGTTCTCT CCGGGTTCTCT CCGGGTTCTCT CCGGGTTCTCT CCGGGTTCTCT	GGG M.in GG M.pa GG M.sc GG M.tu CGG M.bc CGG M.le CGG M.ga	tracellulare ratuberc. rofulaceum berculosis vis prae insasii stri
	49		500	510	520	
129 568 164 116 164 124 179 126 127 160	ATTGACGGTA	AGGTGGAGA AGGTGGAGA AGGTGGAGA AGGTGGAGA AGGTGGAGA AGGTGGAGA AGGTGGAGA AGGTGGAGA AGGTGGAGA	AGAAGCACCAAAGAAGAAGAAGAAGAAGCACCAAGAAGCACCAGAAGCACCAGAAGCACCAGAAGCACCAGAAGCACCAGAAGCACCAC	GGCCAACTACO GGCCAACTACO GGCCAACTACO GGCCAACTACO GGCCAACTACO GGCCAACTACO GGCCAACTACO GGCCAACTACO GGCCAACTACO	TG M.bo TG M.av TG M.in TG M.pa TG M.sc TG M.le TG M.ka TG M.ga TG M.ga	vis ium tracellulare ratuberc. rofulaceum prae nsasii stri rdonae

Figure 5A

Bus. PRG. Burs Budglass

#### 29/31

		γ	——————————————————————————————————————			
	1	130	1140	1150	116	50
1104	TCTCATGT	receaede	GGTAATGCCC	GGGACTCGTGA	3070	
1056	TCTCATGT	recenece.	CCTAATOCCC	CCCACTCGTG	AGAG	M.intracellulare
1098	TCTCATGT	racenace.	GGTAATGCCG GGTAATGCGG	CCCACTCGTG	AGAG	M.intracellulare M.paratuberc.
1064	TOTOMICT	PGCCAGCG	CONTRACCO	GGGACTCGTGA	LGAG	M.paratuberc. M.scrofulaceum
1069	TOTOMIGH	recented.	30 1 AA 1 G C C G	GGGACTCGTGF	AGAG	M.scrofulaceum M.tuberculosis
1208	TOTORIGI	rcccrcch	CONTRACTO	GGGACTCGTG	AGAG	M.tuberculosis
1110	TCICAIGI.	I GCCAGCA	GTAATGGTG	GGGACTCGTGA	AGAG	M.bovis
1066	TCTCATGT,	rgccagc <u>a</u>	GTAATGGTG	GGGACTCGTG	AGAG	M.leprae
1060	TCTCATGT	rgccagcg(	GTAATGCCG	GGGACTCGTG	AGAG	M.kansasii
1100/	TCTCATGT	reccaece	GTAATGCCG	GGGACTCGTG	AGAG	M.gastri
1100	TCTCATGT	r GCCAGCG	GTAATGCCG	GGGACTCGTGA	\GAG	M.gordonae
1001	TCTCATGT	rgccagc <u>a</u>	getaateete	GGGACTCGTGA	AGAG	M.marinum
		T				
		290	1300	1310	132	-
1264	CGAATCCTT	TTAAAGCC	CGGACTCAGT	TCGGATTEGGG	TCT	M. avium
1216	CGAATCCTT	TTAAAGCO	CGGTCTCAGT	TCGGATTGGGG	ТСТ	M.intracellulare
1258	CGAATCCTI	TTAAAGC	CGGACTCAGT	ТСССАТТСССС	יחיטיתי	M neretubera
1224	CGAATCCTT	TTAAAGC	CGGTCTCAGT	rcggatdgggg	тст	M. scrofulaceum
1229	CGAATCCTT	A-AAAGCO	CGGTCTCAGT	TCGGATCGGGG	mcm	M.tuberculosis
1368	CGAATCCTT	a-laaagco	CGGTCTCAGT	TCGGATCGGGG	TOT.	M hovis
1279	CGAATCCTT	TTAAAGCC	CGGTCTCAGT	rcggatogggg	TOT.	M lenrae
1226	CGAATCCTT	TTAAAGCC	CGGTCTCAGT	rcggatgggg	TOT	M kangagii
1227	CGAATCCTT	TTAAAGCC	GGTCTCAGT	rcggateggg	TOT	M castri
1260	CGAATCCTT	TTAAAGCC	CGCTCTCAGT	rcggateggg	TC1	M gordonao
1221	CGAATCCTT	TEAAAGCC	GGTCTCAGT	rcggatogggg	mcm TCT	M maninum
			OUTONOT.	reaght Maaga	101	M. Macinum
	1 -	330	1240	1050		_
1001			1340	1350	136	
1304	GCAACTCGA	CCCCATGA	AGTCGGAGT	CGCTAGTAATC	GCA	M.avium
1256	GCAACTCGA	CCCCATGA	AGTCGGAGT	CGCTAGTAATC	GCA	M.intracellulare
1298	GCAACTAGA	CCCAATGA	AGTCGGAGT	CGCTAGTAATC	GCA	M.paratuberc.
1264	GCAACTCGA	CCCCGTGA	AGTCGGAGT	CGCTAGTAATC	GCA	M.scrofulaceum
1268	GCAACTCGA	CCCCGTGA	AGTCGGAGT	CGCTAGTAATC	GCA	M.tuberculosis
1407	GCAACTCGA	CCCCGTGA	AGTCGGAGT	CGCTAGTAATC	GCA	M.bovis
1319	GCAACTCGA	CCCCGTGA	AGTCGGAGT	CGCTAGTAATC	GCA	M.leprae
1266	GCAACTCGA	CCCGTGA	AGTCGGAGT	CGCTAGTAATC	GCA	M.kansasii
1267	GCAACTCGA	CCCCGTGA	AGTCGGAGTC	CGCTAGTAATC	GCA	M.gastri
1300	GCAACTCGA	CCCGTGA	AGTCGGAGTC	CGCTAGTAATC	GCA	M.gordonae
1260	GCAACTCGA	CCCCGTGA	AGTCGGAGTC	CGCTAGTAATC	GCA	M marinum

## Figure 5B

M.avium 23S.

Figure 6

Figure 7

M. tuberculosis 16S: